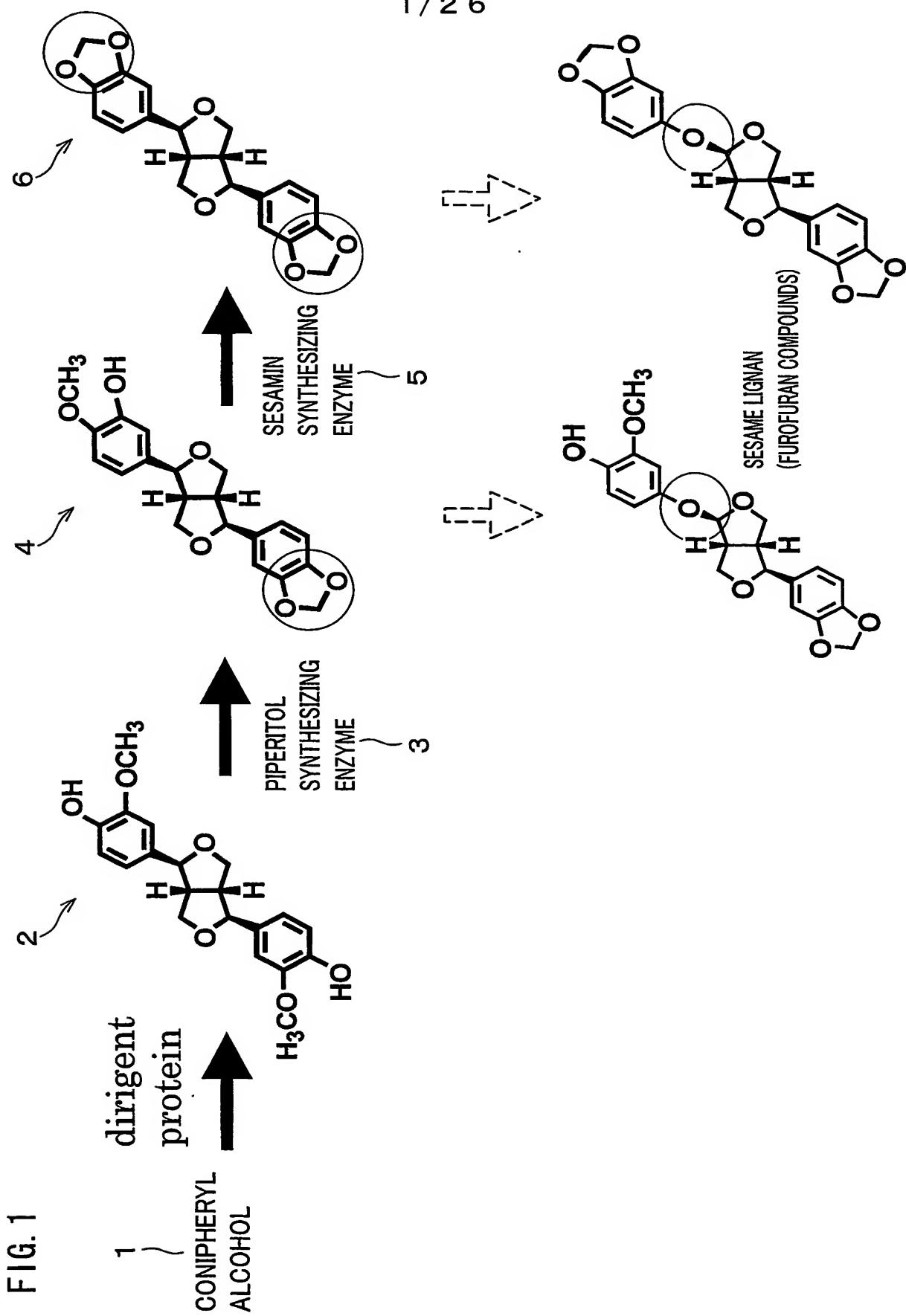


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FIG. 2 (a) pYE22m / PINORESINOL

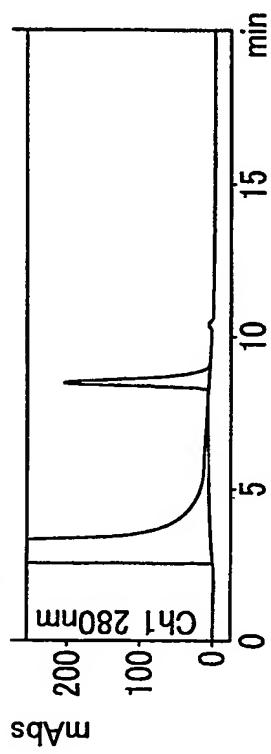


FIG. 2 (d) pYE22m / PIPERITOL

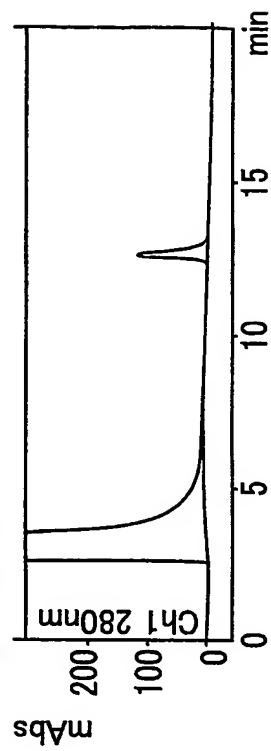


FIG. 2 (b) SiP189 / PINORESINOL

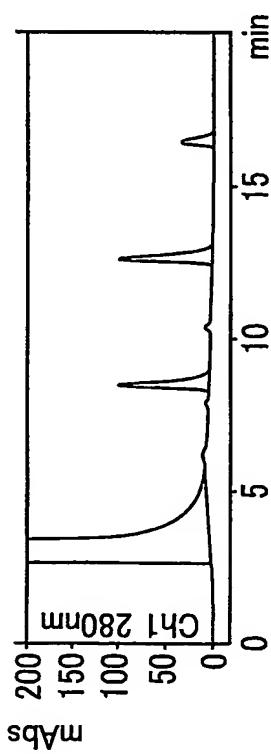


FIG. 2 (e) SiP189 / PIPERITOL

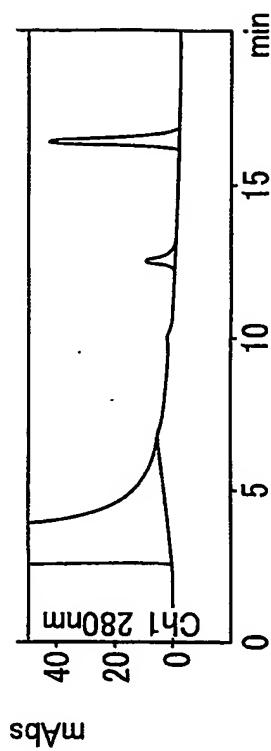


FIG. 2 (c) SiP189 / PINORESINOL

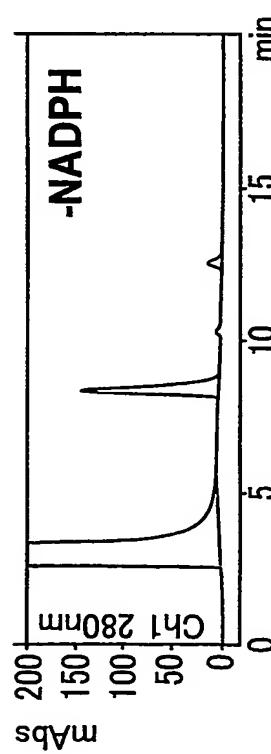
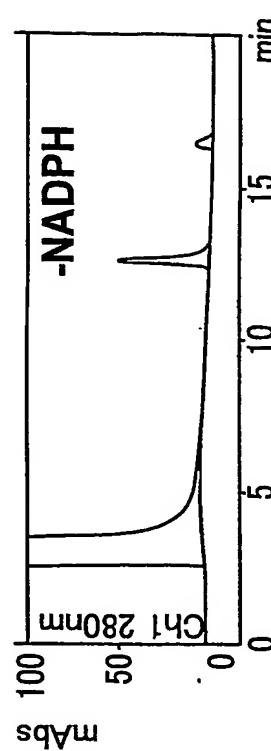
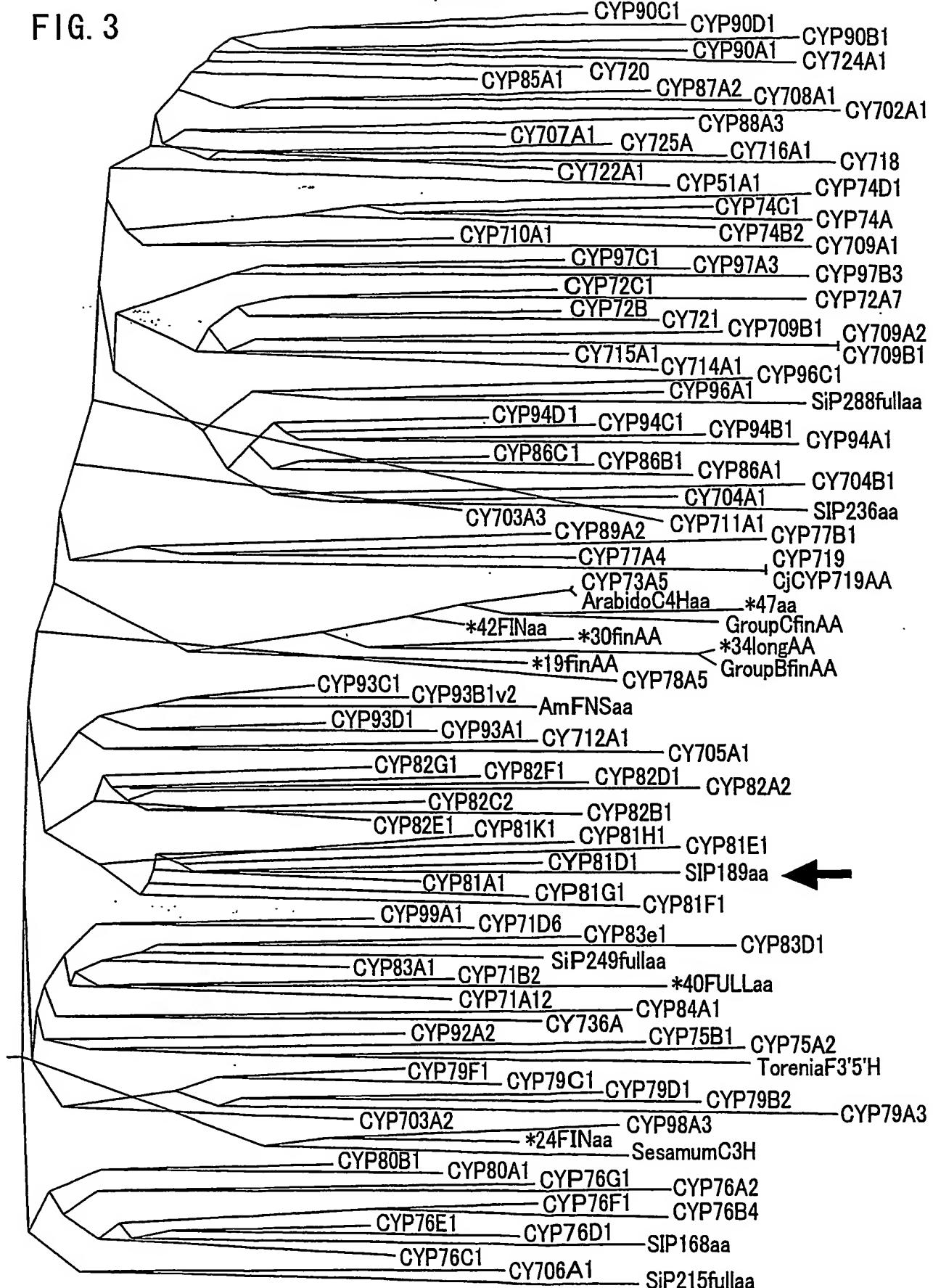


FIG. 2 (f) SiP189 / PIPERITOL



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FIG. 3



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FIG. 4

> Blastx Search (SST vs PIR)

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= BXP184.2003.08.12
(1521 letters)

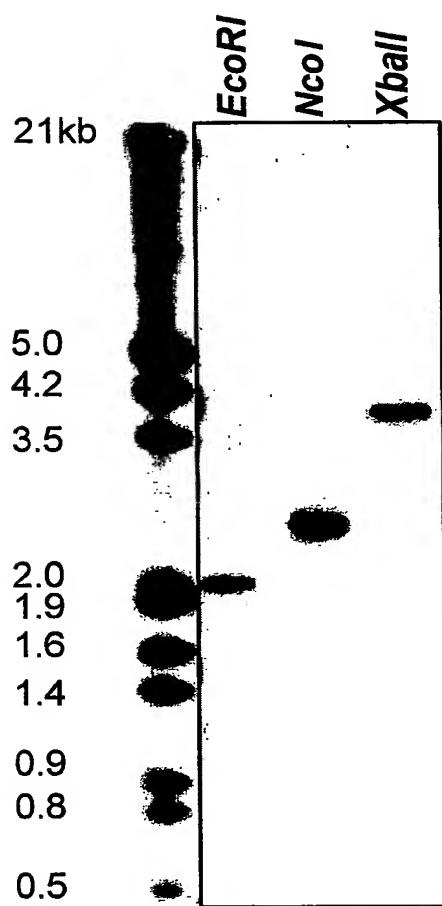
Database: pir1.fasta; pir2.fasta; pir3.fasta; pir4.fasta
283,329 sequences; 96,175,589 total letters

Searching.....done

		Score	E
		(bits)	Value
Sequences producing significant alignments:			
T04730	(PIR) cytochrome P450 homolog F6G17.10 - Arabidopsis thal...	494	e-139
C85441	(PIR) cytochrome P450-like protein [imported] - Arabidopsis	494	e-139
T52174	(PIR) cytochrome P450 monooxygenase [imported] - Arabidopsis	487	e-137
B85441	(PIR) cytochrome P450-like protein [imported] - Arabidopsis	481	e-135
T04731	(PIR) cytochrome P450 homolog F6G17.20 - Arabidopsis thal...	480	e-135
T10896	(PIR) cytochrome P450 (EC 1.14.-.-) 81B1c - Jerusalem art...	468	e-131
A85441	(PIR) cytochrome P450-like protein [imported] - Arabidopsis	464	e-130
T00510	(PIR) probable cytochrome P450 At2g23220 [imported] - Ara...	457	e-128
T00513	(PIR) cytochrome P450 homolog At2g23190 - Arabidopsis tha...	453	e-127
B96691	(PIR) probable cytochrome P450 F28G11.4 [imported] - Arab...	444	e-124

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FIG. 5



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FIG. 6 (a) SrSiP189/ PINORESINOL

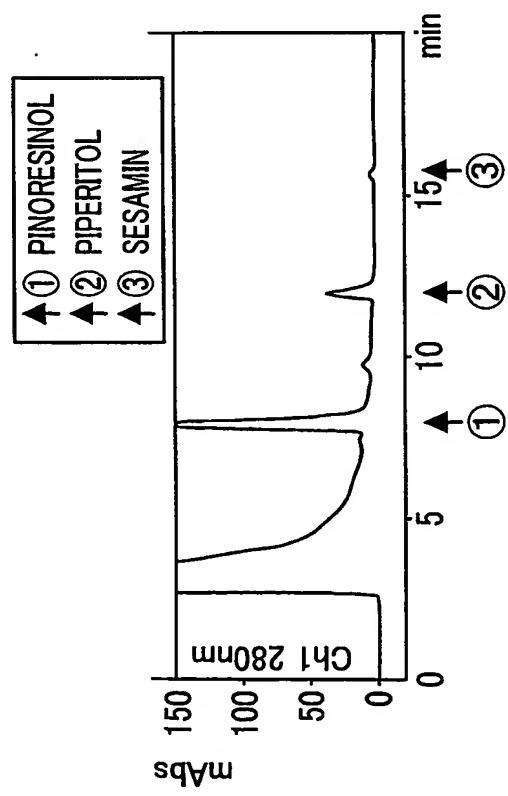


FIG. 6 (b) SrSiP189/ PIPERITOL

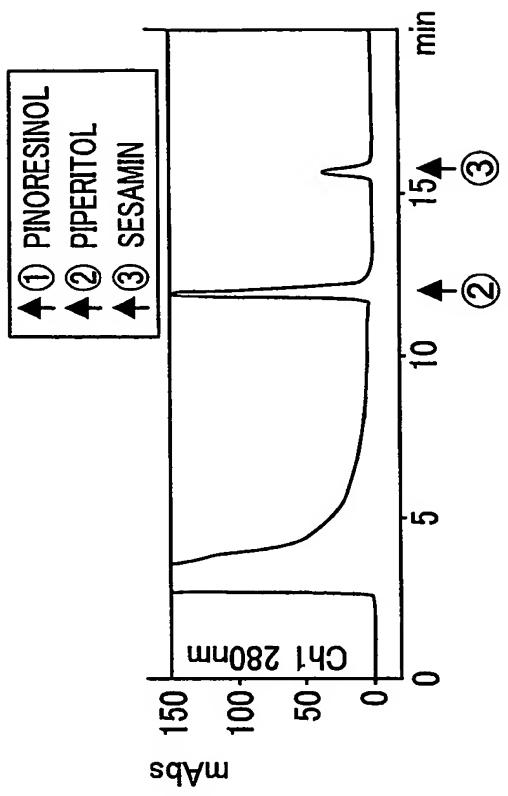


FIG. 6 (c) SrSiP189/ PINORESINOL

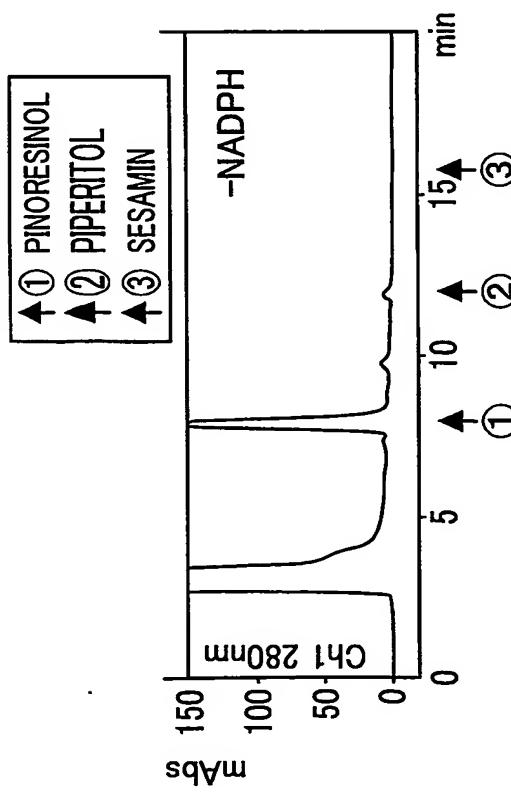
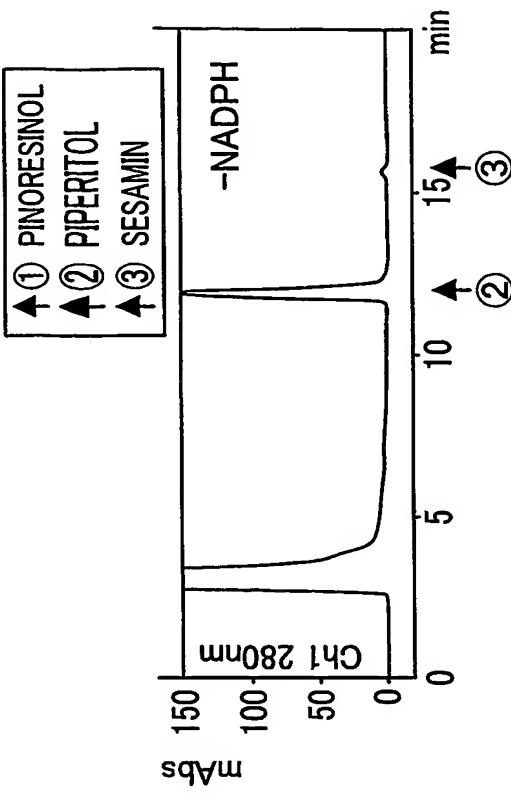


FIG. 6 (d) SrSiP189/ PIPERITOL



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FIG. 7

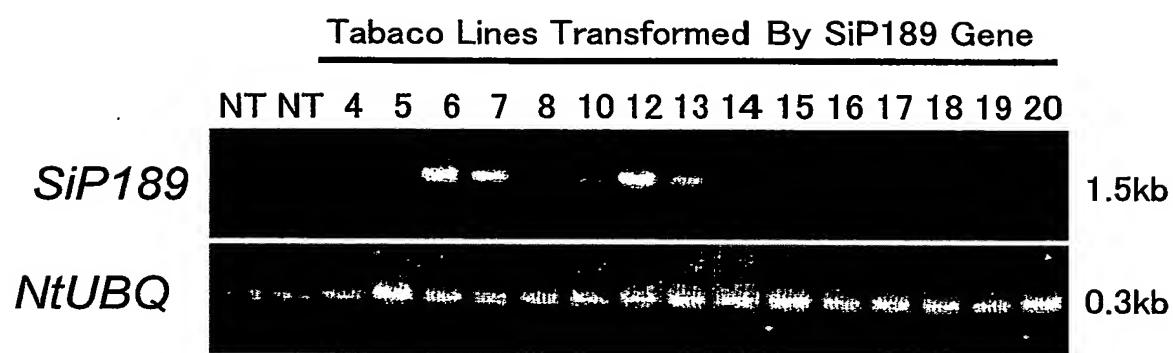
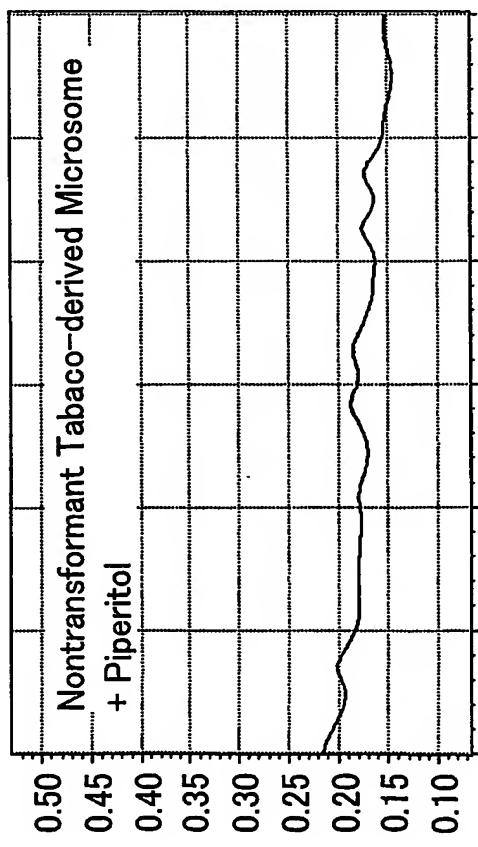
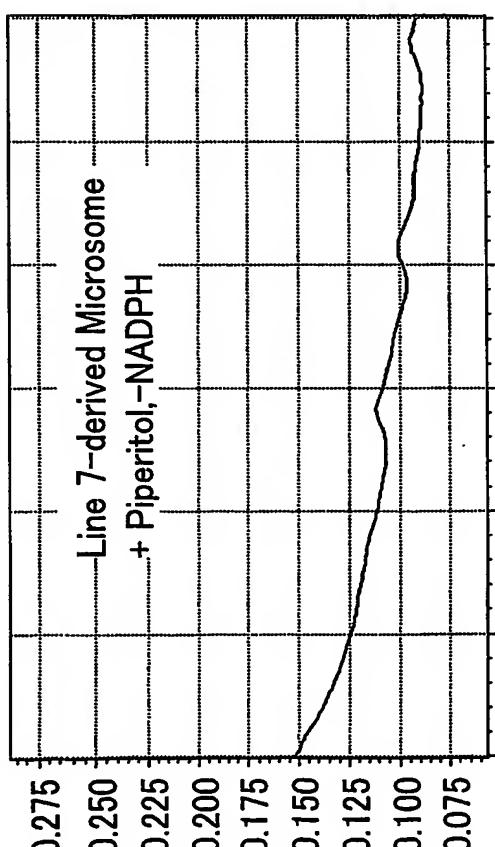


FIG. 8 (a)



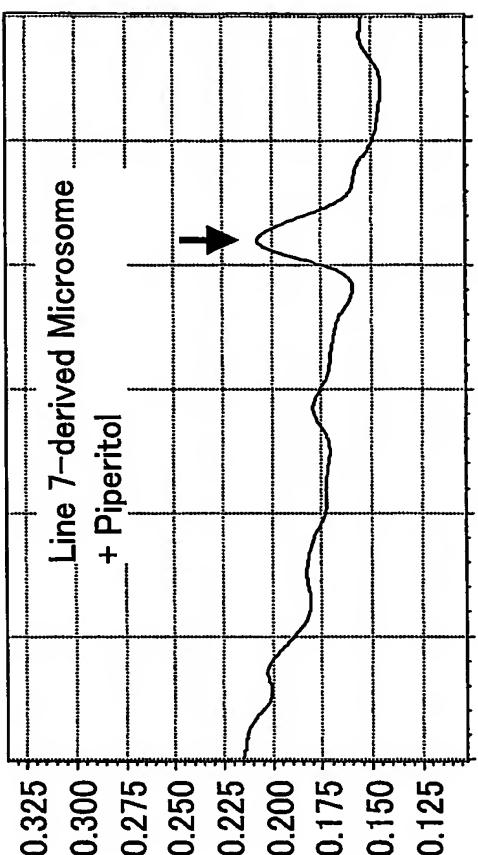
15.0 15.5 16.0 16.5 17.0 17.5 分

FIG. 8 (c)



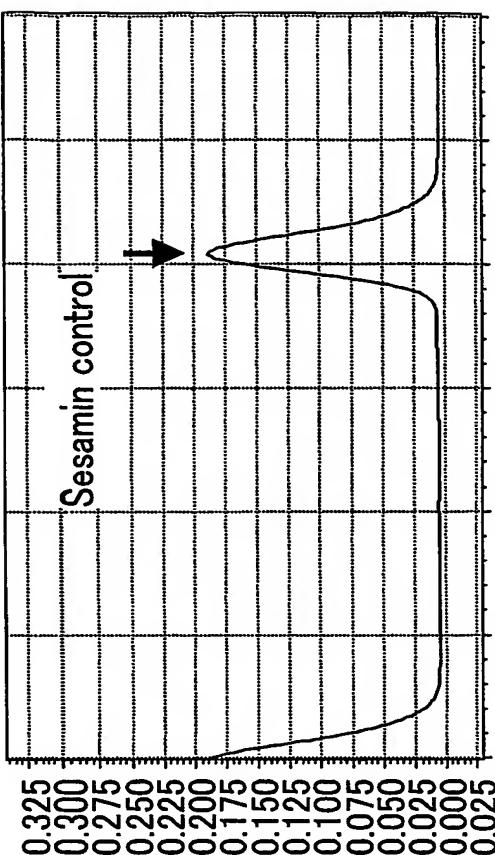
15.0 15.5 16.0 16.5 17.0 17.5 分

FIG. 8 (b)



15.0 15.5 16.0 16.5 17.0 17.5 分

FIG. 8 (d)

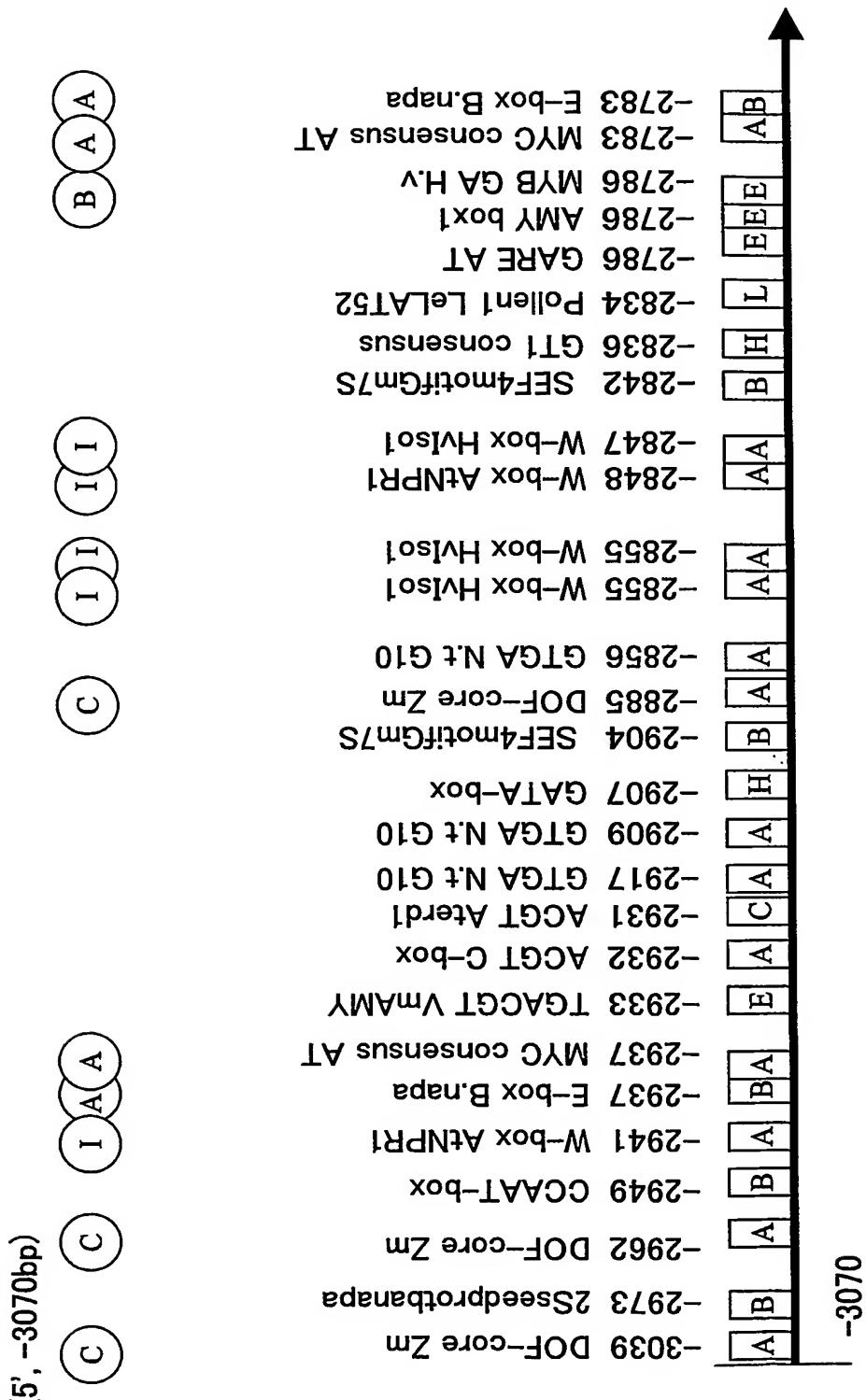


15.0 15.5 16.0 16.5 17.0 17.5 分

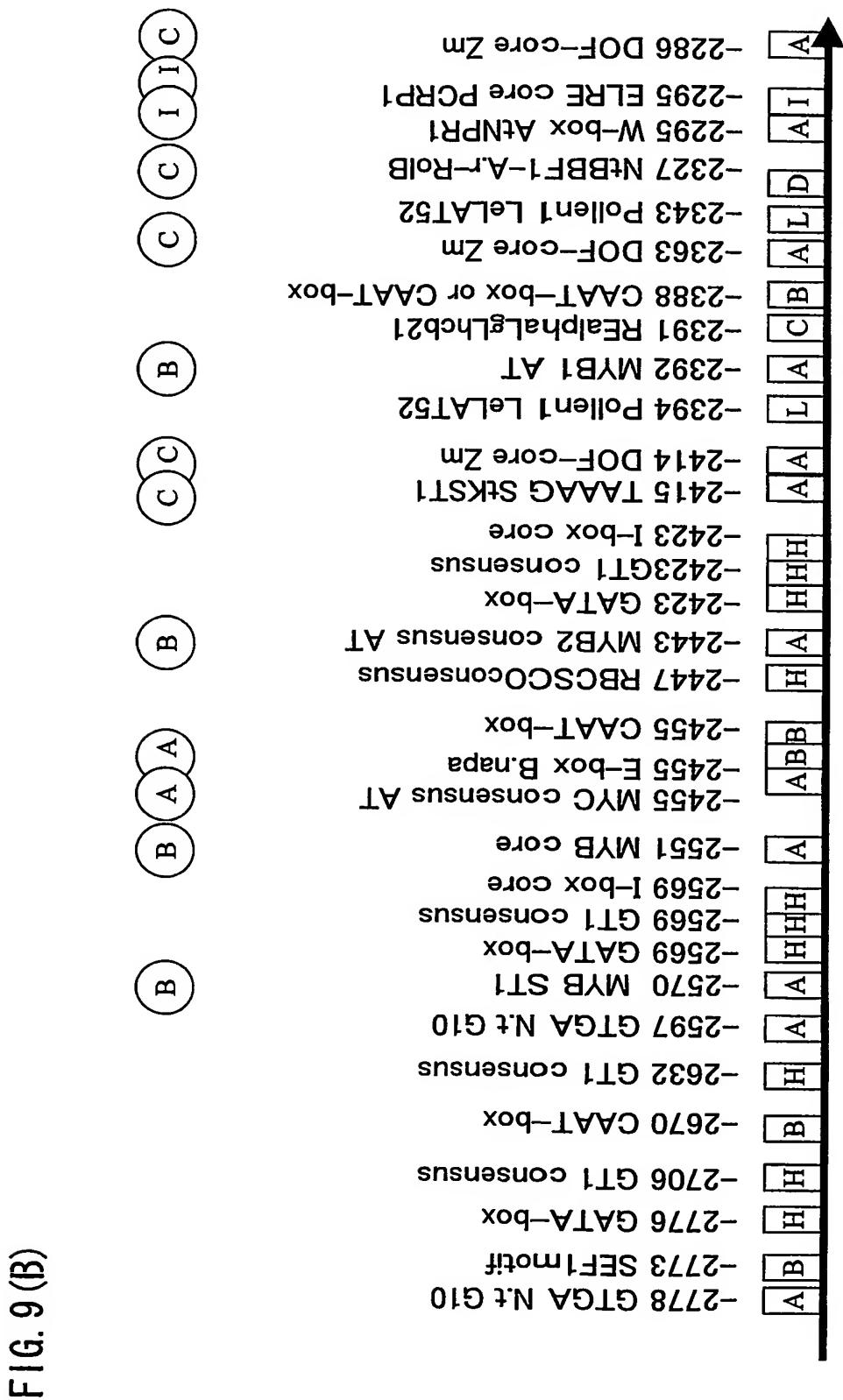
8 / 2 6

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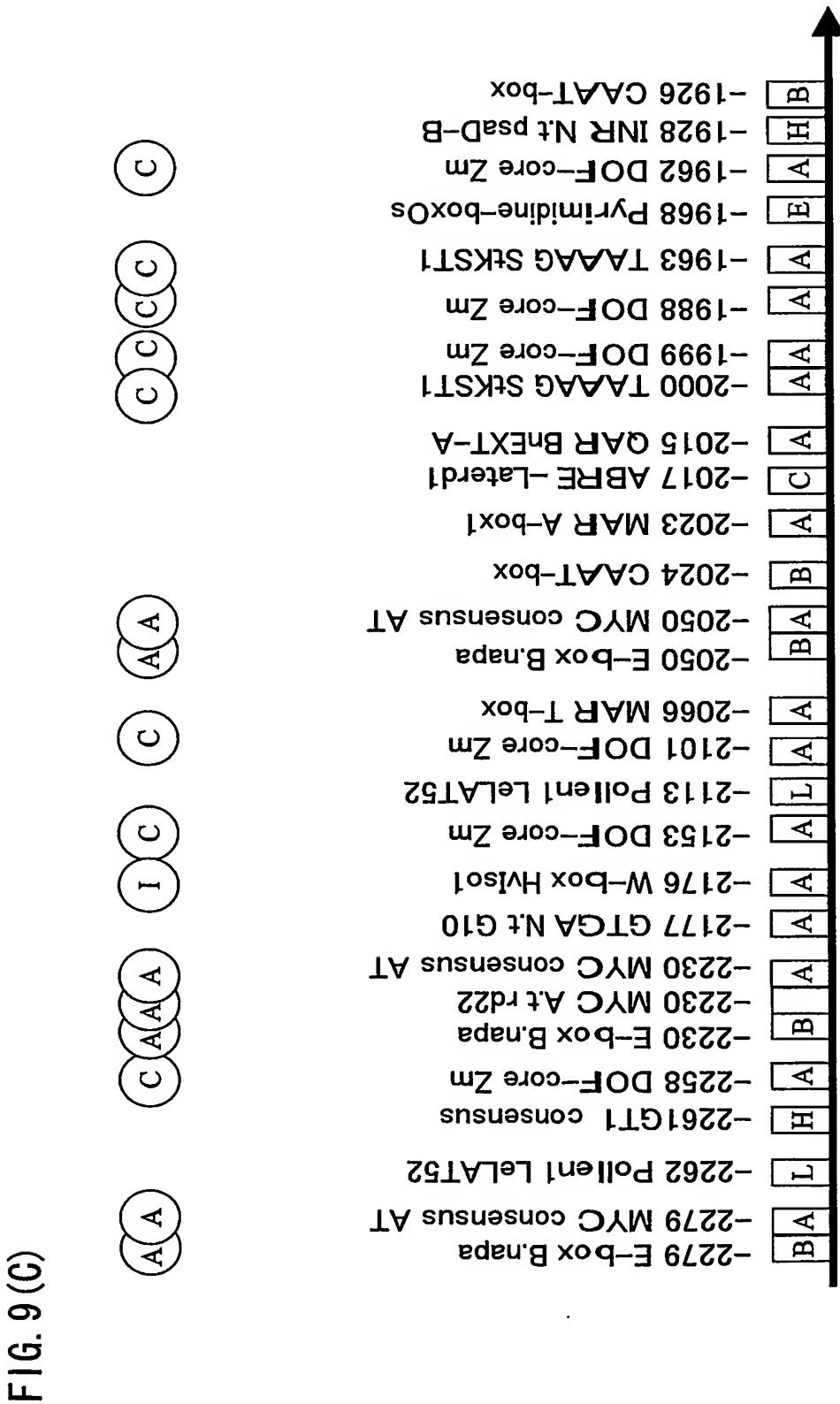
FIG. 9 (A)



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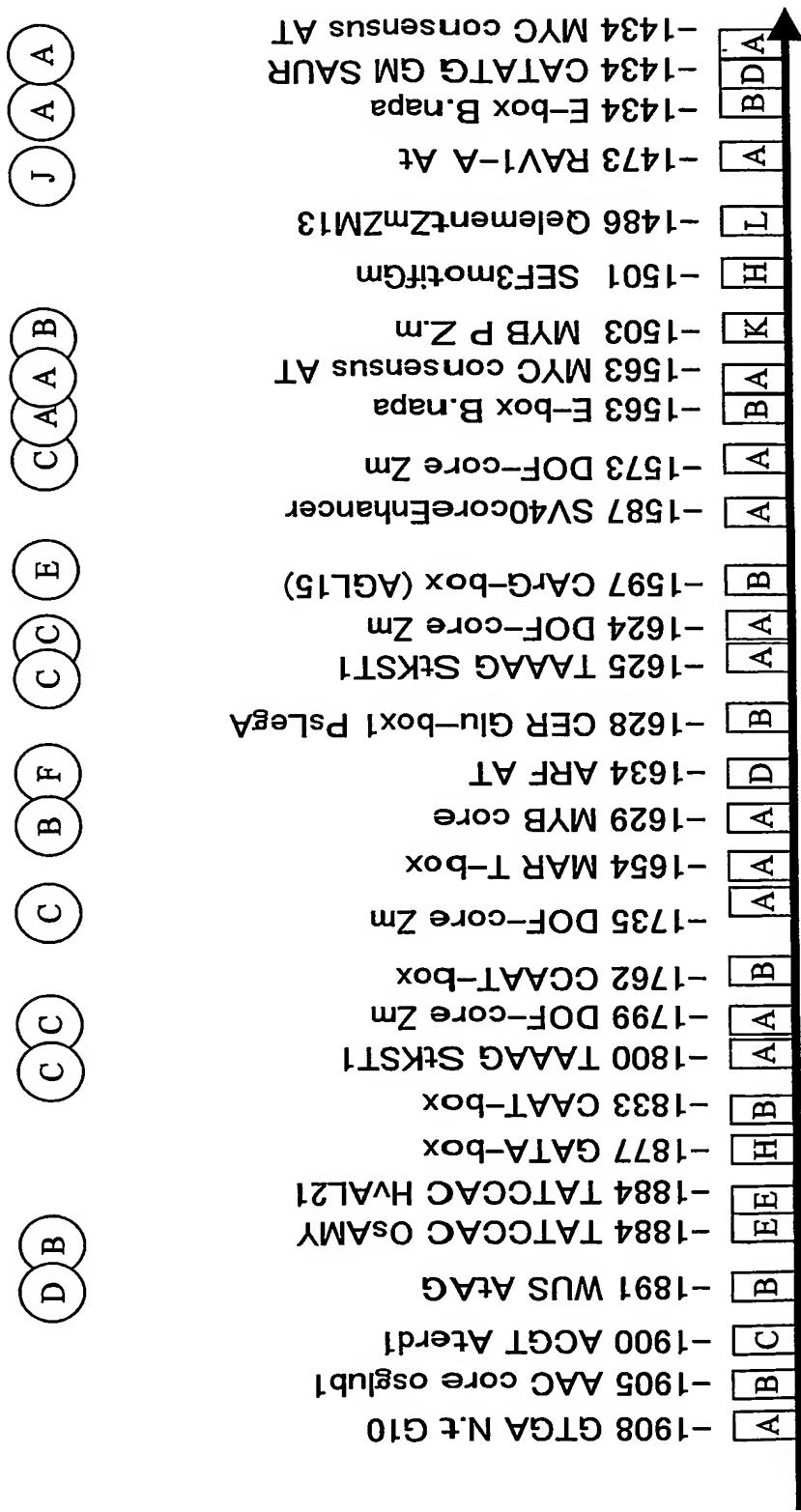


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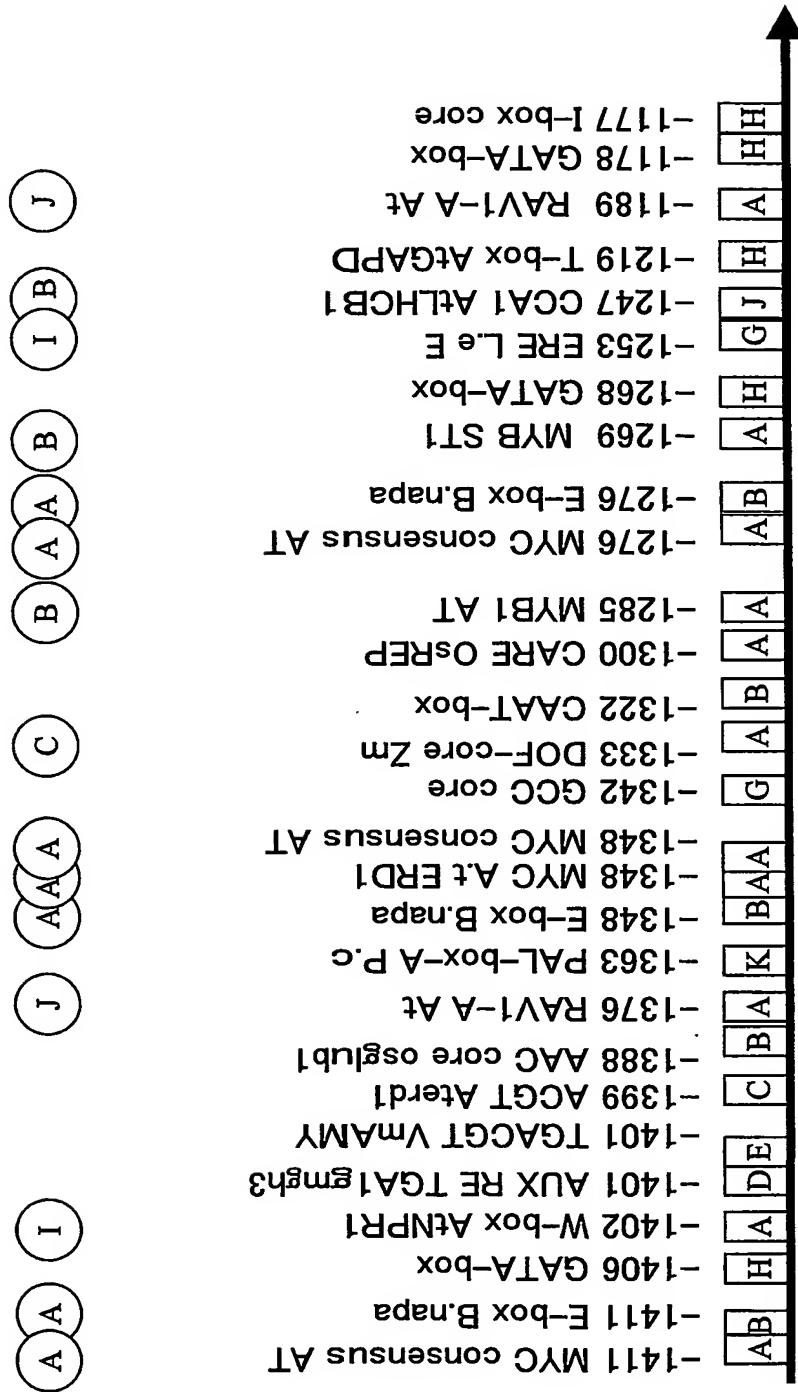
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FIG. 9 (D)



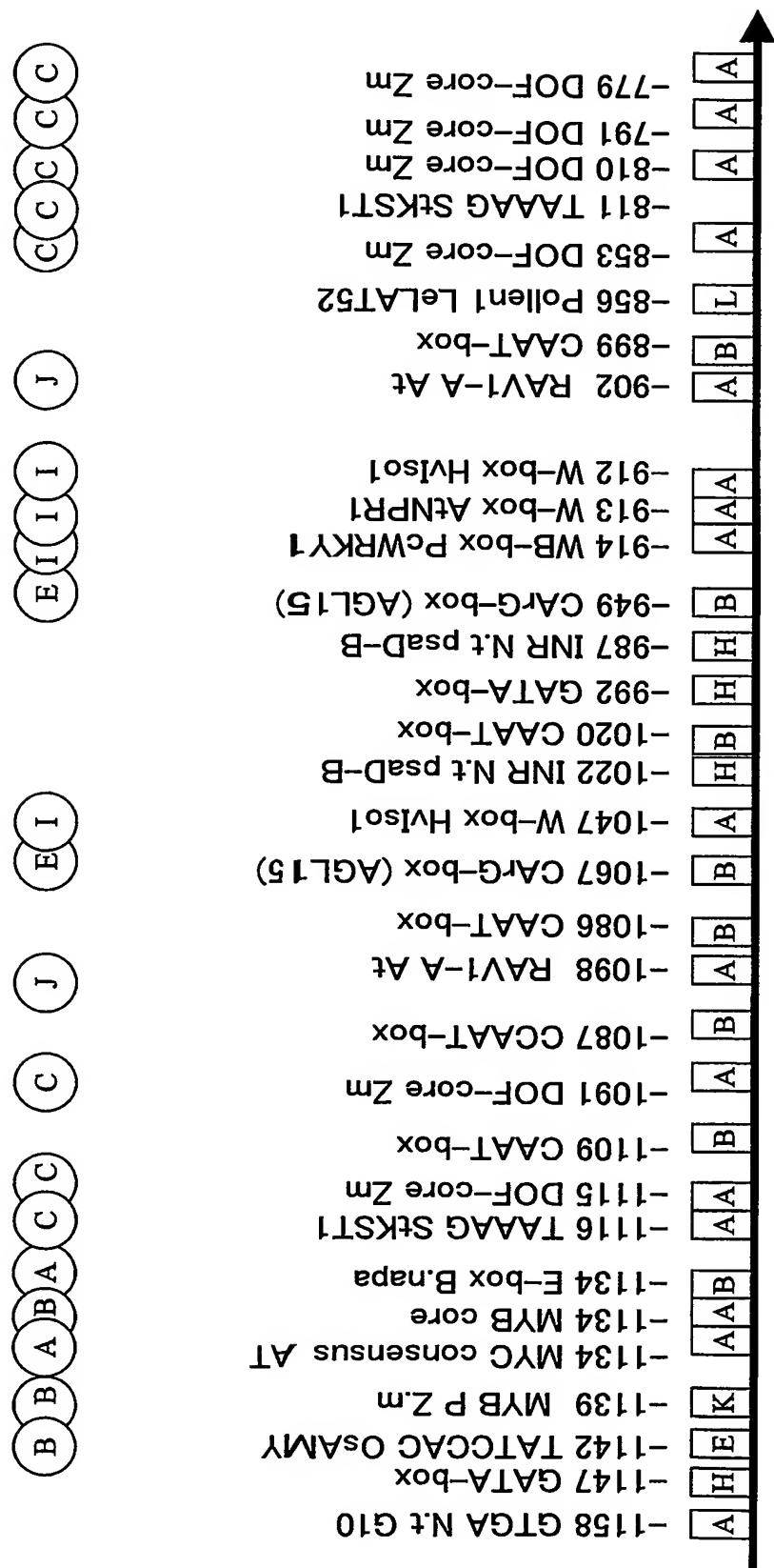
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FIG. 9 (E)



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FIG. 9(F)



1 5 / 2 6

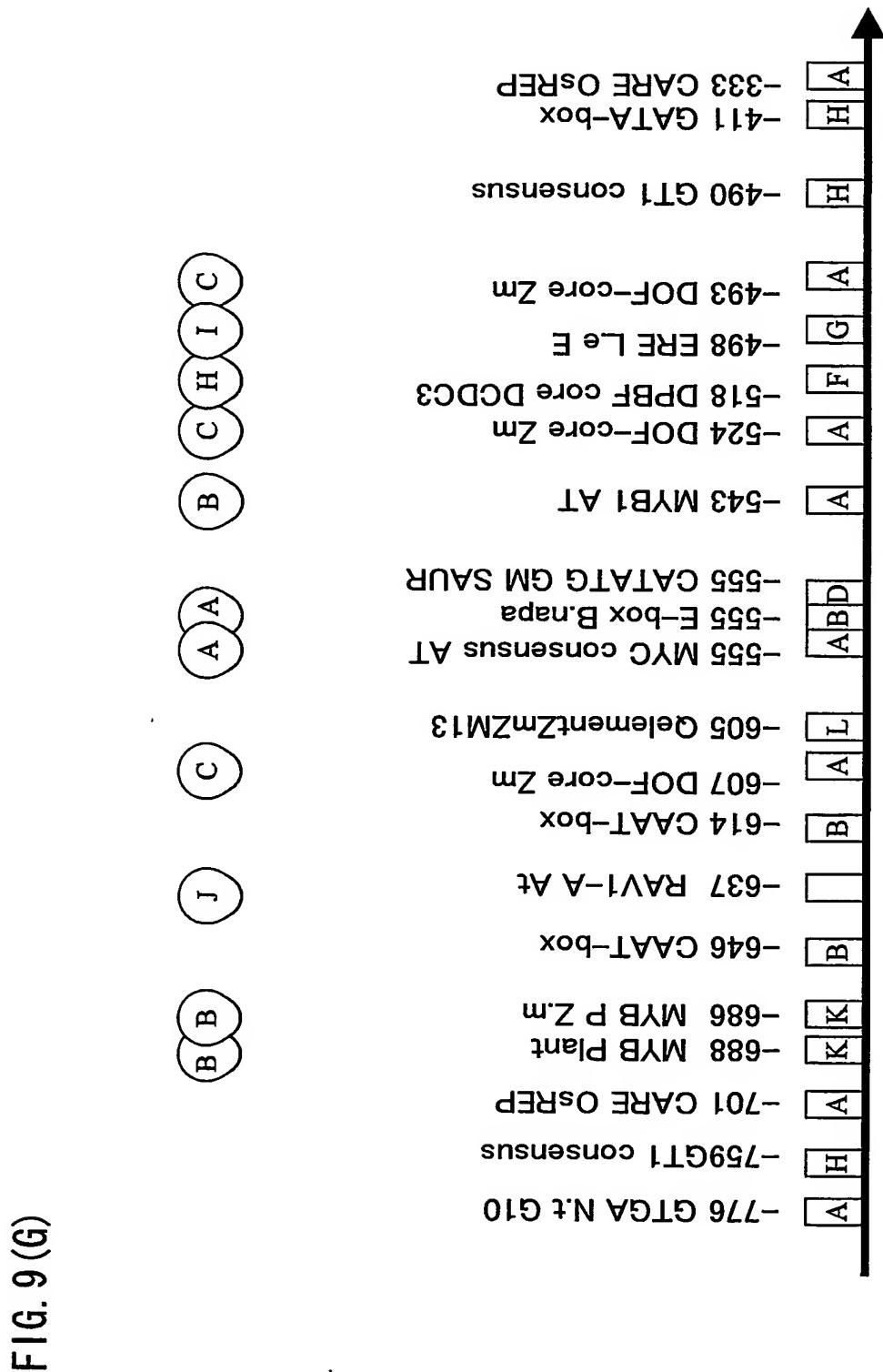
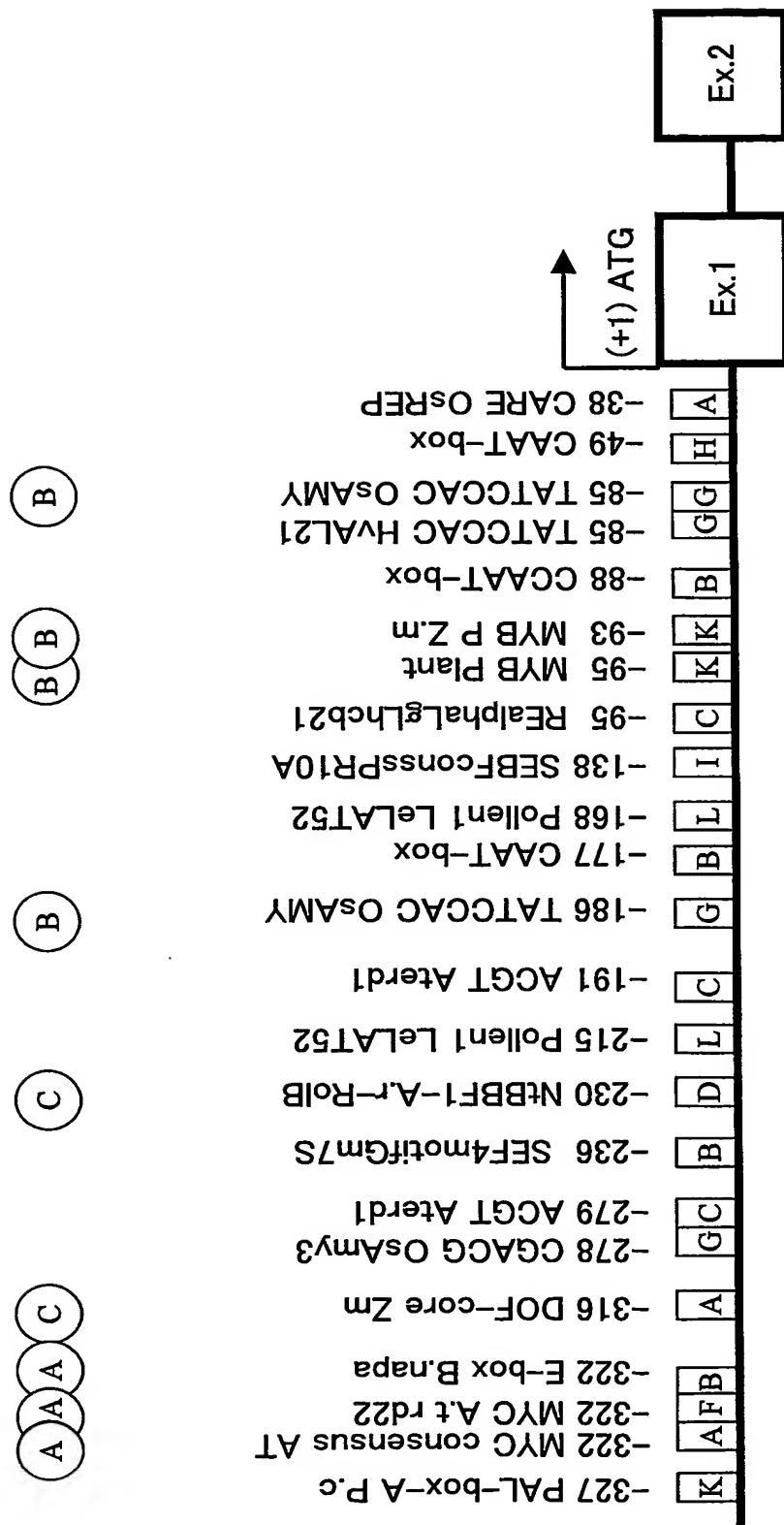


FIG. 9 (G)

1 6 / 9 1

FIG. 9 (H)



1 7 / 2 6

FIG. 10

Putative Physiological response

- [A] Unknown
- [B] Seed/endosperm/embryo-related
- [C] Etiolation-related
- [D] Auxin-related
- [E] GA/amylase-related
- [F] ABA-related
- [G] Ethylen-related
- [H] Light-regulated
- [I] Pathogenesis-related
- [J] Circadian clock-regulated
- [K] Secondary metabolism-related
- [L] Pollen development

Putative structure of target *trans*-factor

- (A) Myc (bHLH class)
- (B) Myb
- (C) Zinc Finger (Dof class)
- (D) Homeobox
- (E) MADS
- (F) ARF
- (G) Leucine Zipper (TGA class)
- (H) bZIP (DPBF class)
- (I) WRKY
- (J) AP2-domain (RAV class)

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FIG. 11 (A)

2815bp

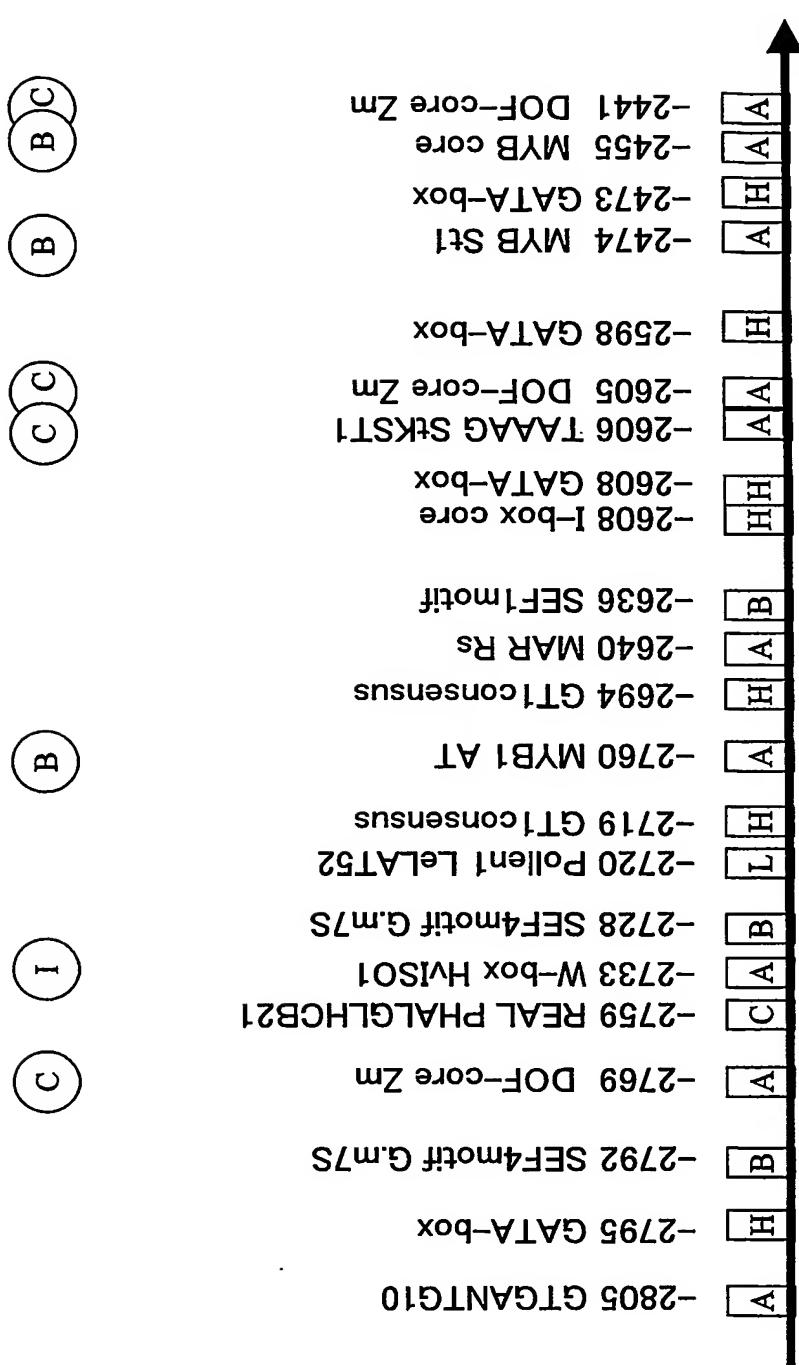
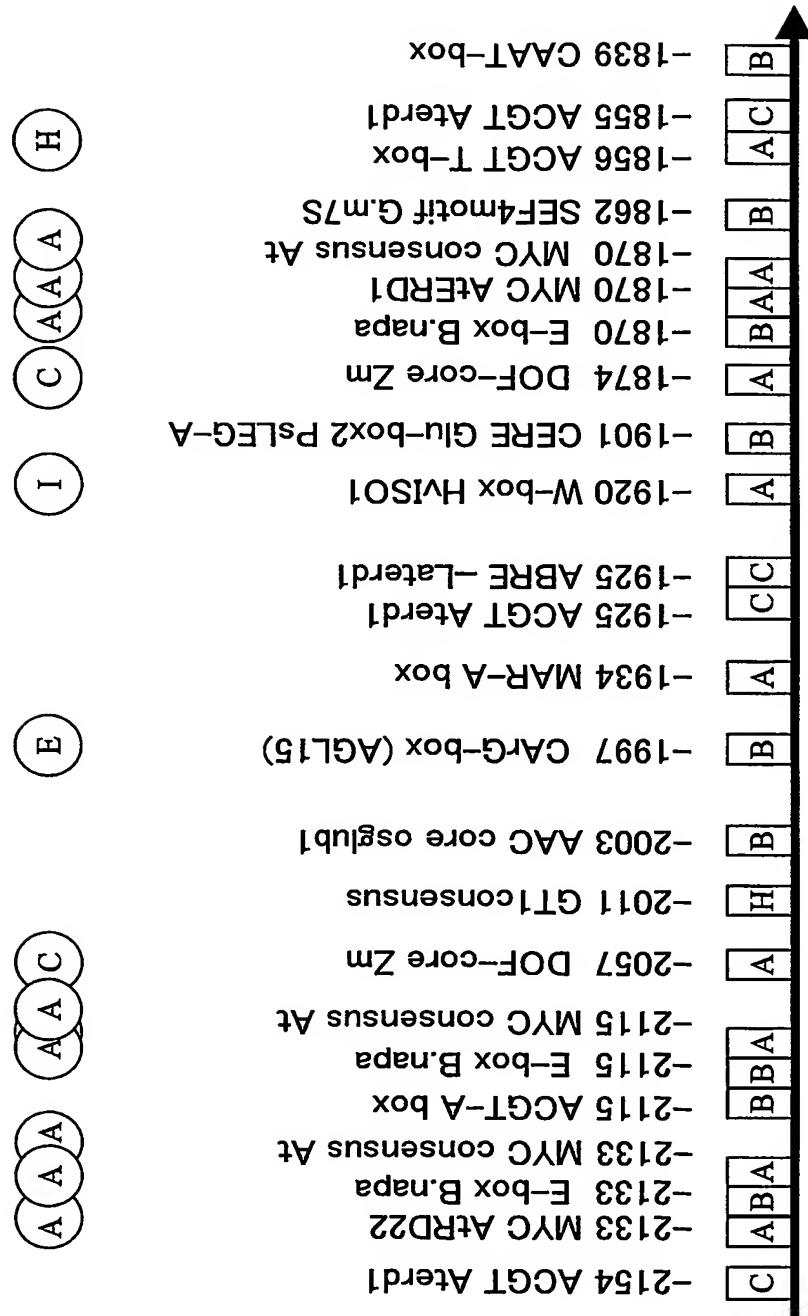


FIG. 11 (B)

-2408 GT1 consensus	B	H
-2408 GATA-box		
-2408 I-box core		
-2380 CAAT-box	B	
-2358 MYB2 consensus AT	A B A	I
-2358 E-box B-napa		
-2358 MYC consensus At		
-2328 W-box ATNPR1		
-2311 Circadian LeLHC	J	
-2292 GCAT-box1	A B	
-2291 CAAT-box		
-2275 ACCT Aterdi	C	
-2270 DOF-core Zm	A	
-2245 GT1 consensus	H	
-2207 TAAAG STKST1	A A	L
-2206 DOF-core Zm		
-2204 Pollen1 LeLAT52		
-2203 GT1 consensus	H H	
-2198 EREcore PCR1	I I	
-2198 W-box ATNPR1		
-2191 DOF-core Zm	A	
-2186 GATA-box	H	

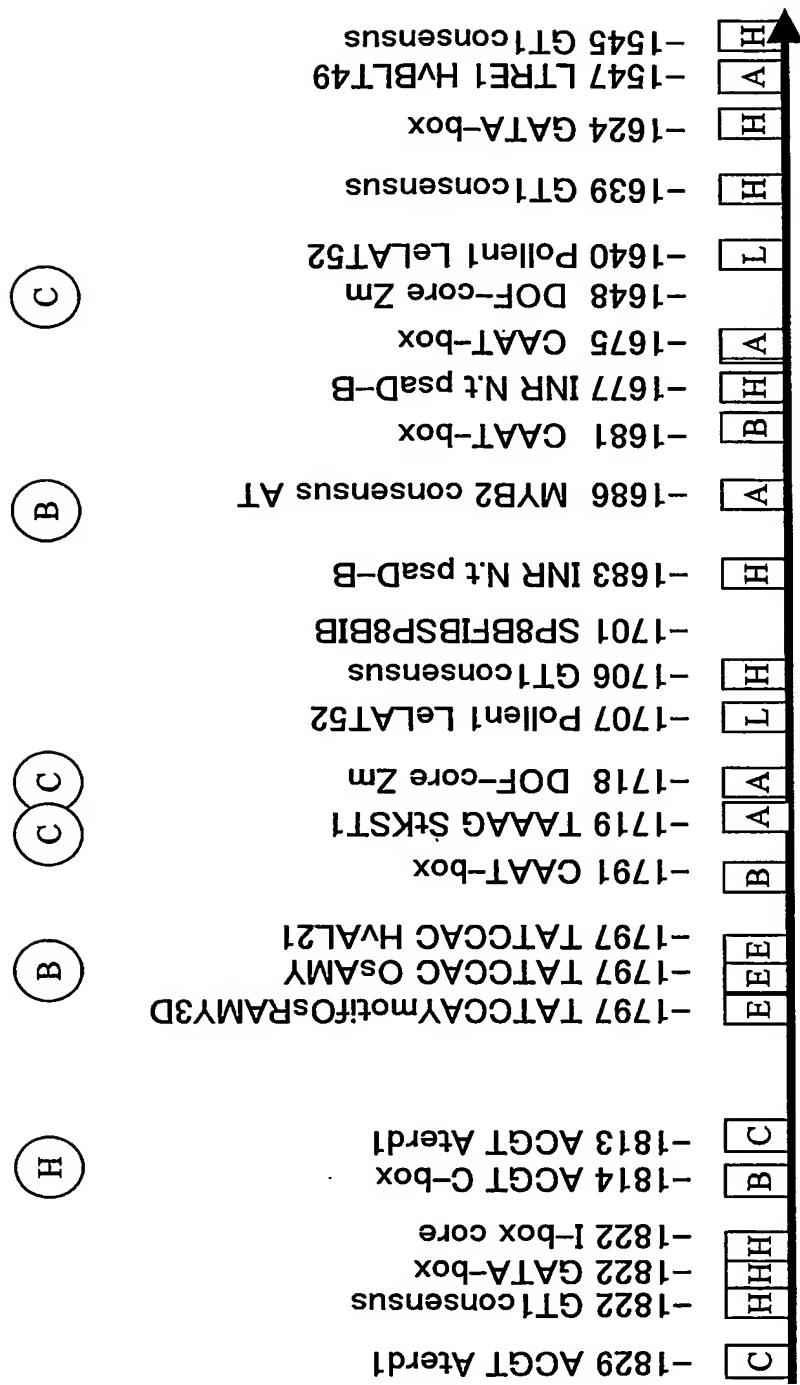
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FIG. 11(C)



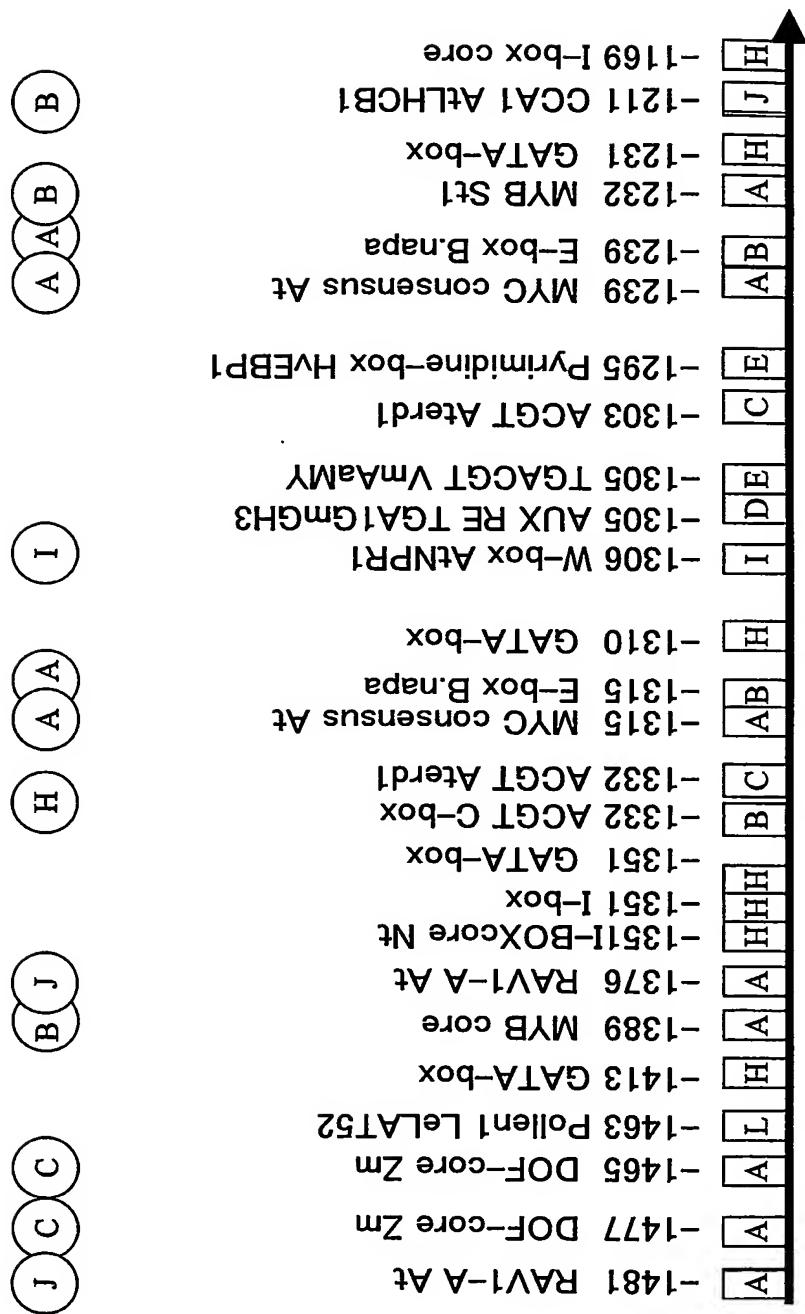
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FIG. 11 (D)



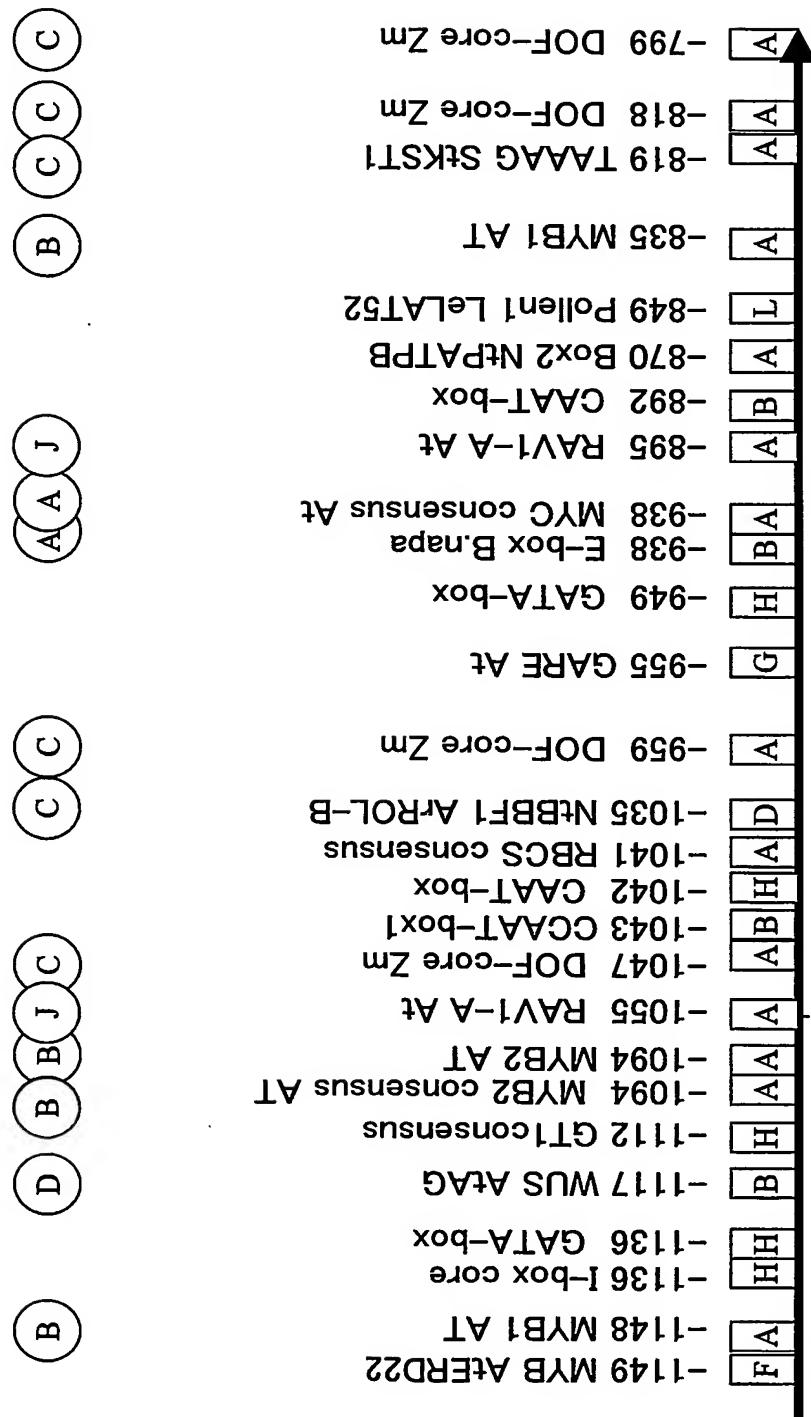
2 2 / 2 2

FIG. 11 (E)



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FIG. 11 (F)



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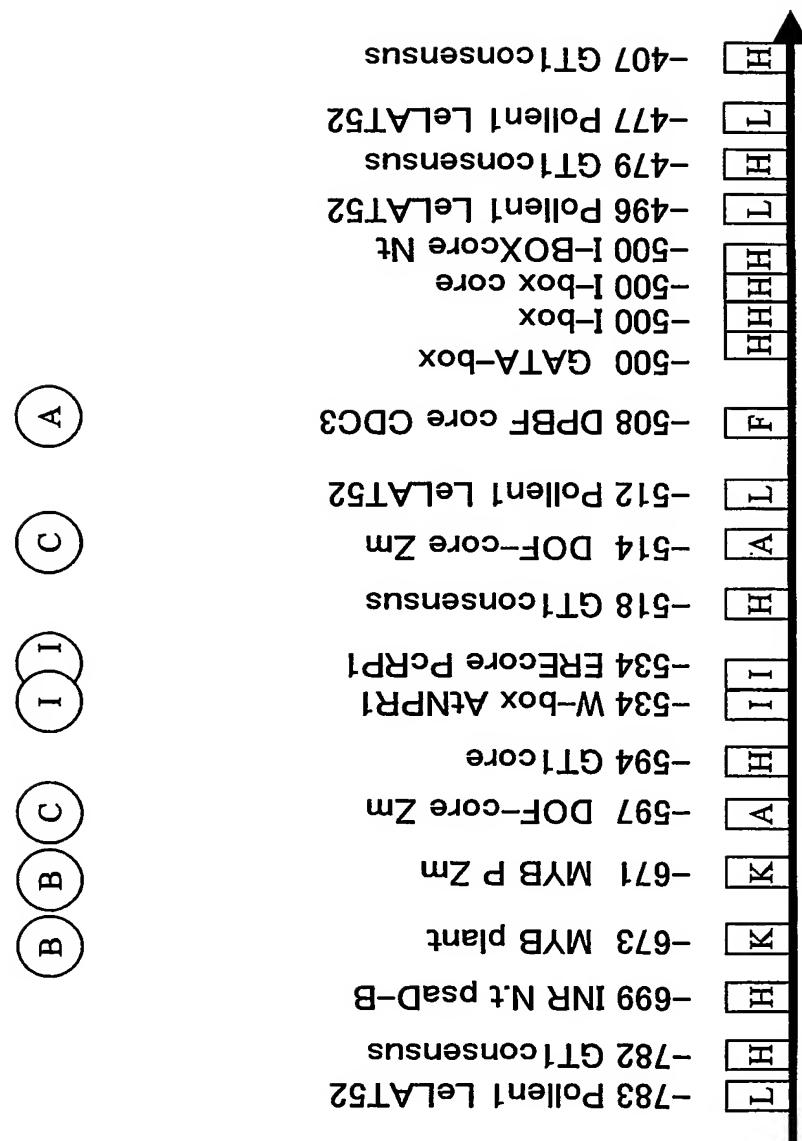
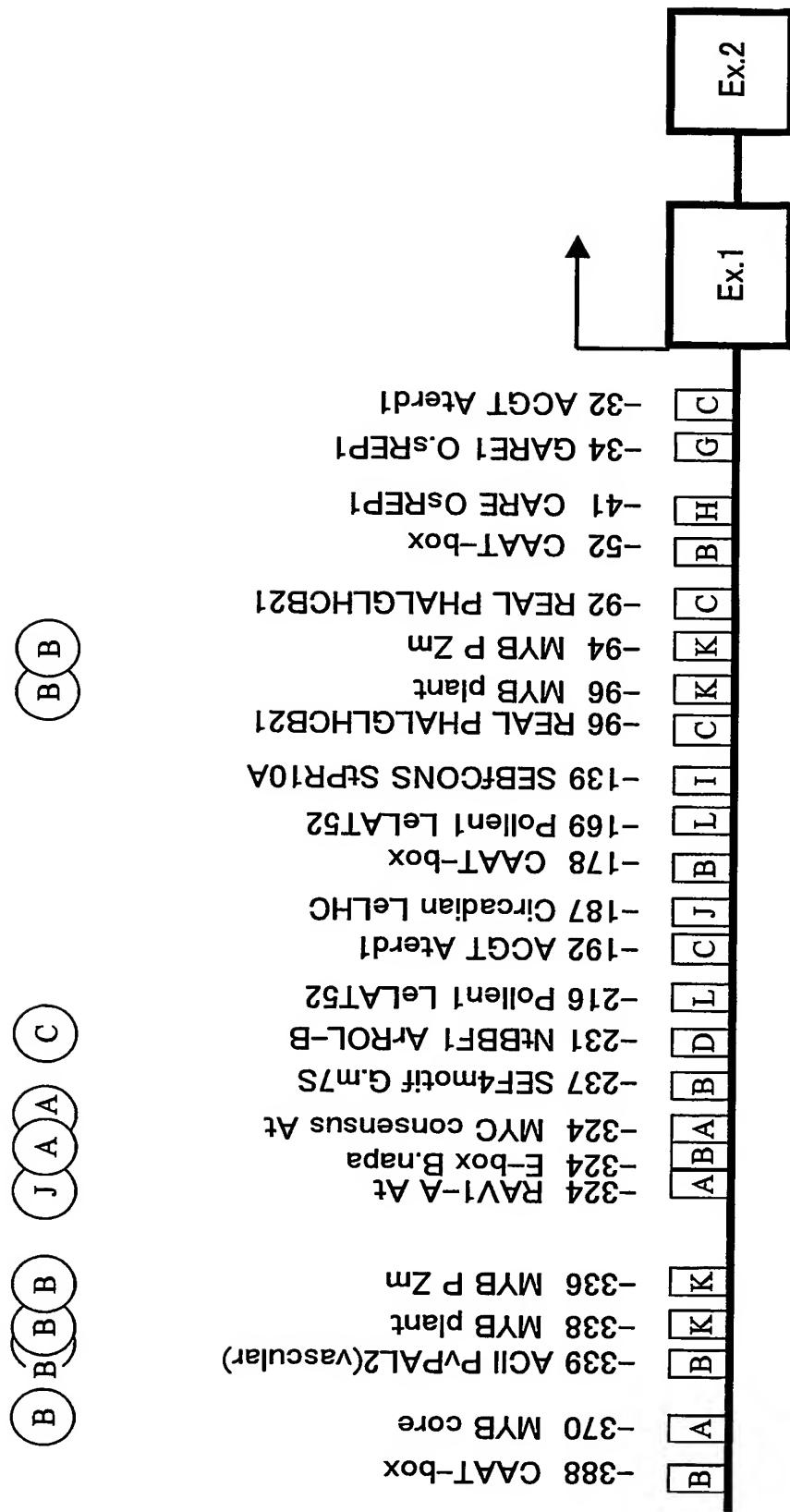


FIG. 11 (G)

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FIG. 11 (H)



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FIG. 12 (a)

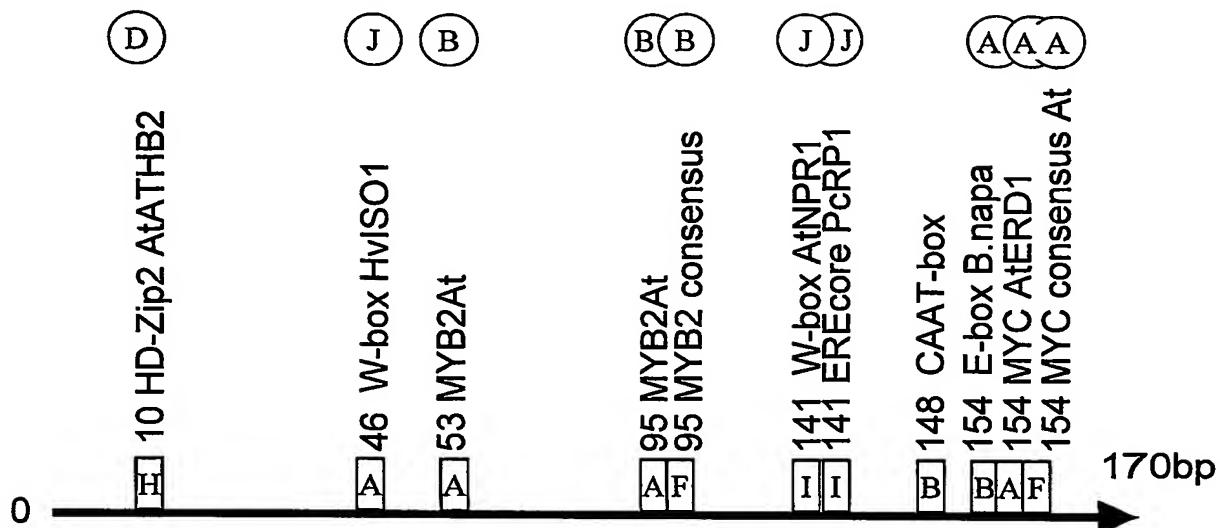
1st Intron of SST (*S.indicum*)

FIG. 12 (b)

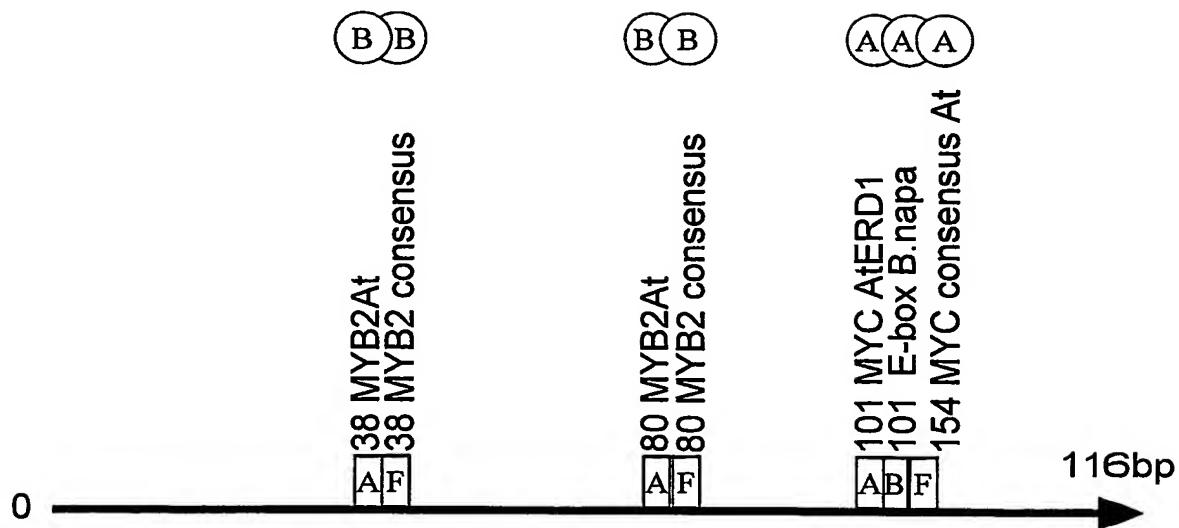
1st Intron of SrSST (*S.radiatum*)

FIG. 12 (c)

